

SEQUENCE LISTING

<110> Fan, Hao
Wei, Zhong-Min

<120> HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
THEREOF

<130> 21829/81

<140>

<141>

<150> 60/212,211

<151> 2000-06-16

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 338

<212> PRT

<213> *Erwinia chrysanthemi*

<400> 1

Met	Gln	Ile	Thr	Ile	Lys	Ala	His	Ile	Gly	Gly	Asp	Leu	Gly	Val	Ser
1				5					10					15	

Gly	Leu	Gly	Ala	Gln	Gly	Leu	Lys	Gly	Leu	Asn	Ser	Ala	Ala	Ser	Ser
			20					25					30		

Leu	Gly	Ser	Ser	Val	Asp	Lys	Leu	Ser	Ser	Thr	Ile	Asp	Lys	Leu	Thr
		35					40					45			

Ser	Ala	Leu	Thr	Ser	Met	Met	Phe	Gly	Gly	Ala	Leu	Ala	Gln	Gly	Leu
	50					55					60				

Gly	Ala	Ser	Ser	Lys	Gly	Leu	Gly	Met	Ser	Asn	Gln	Leu	Gly	Gln	Ser
65					70					75					80

Phe	Gly	Asn	Gly	Ala	Gln	Gly	Ala	Ser	Asn	Leu	Leu	Ser	Val	Pro	Lys
				85					90					95	

Ser	Gly	Gly	Asp	Ala	Leu	Ser	Lys	Met	Phe	Asp	Lys	Ala	Leu	Asp	Asp
			100					105					110		

Leu	Leu	Gly	His	Asp	Thr	Val	Thr	Lys	Leu	Thr	Asn	Gln	Ser	Asn	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met		
130	135	140
Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly		
145	150	155
Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly		
165	170	175
Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu		
180	185	190
Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala		
195	200	205
Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val		
210	215	220
Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp		
225	230	235
Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp		
245	250	255
Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys		
260	265	270
Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln		
275	280	285
Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr		
290	295	300
Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala		
305	310	315
Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala		
325	330	335
Asn Ala		

<210> 2
 <211> 2141
 <212> DNA

<213> *Erwinia chrysanthemi*

<400> 2

cgatttttacc cgggtgaacg tgctatgacc gacagcatca cgggtattcga caccgttacg 60
gcgttttatgg ccgcgatgaa ccggcatcag gcggcgcgct ggtcgcgcga atccggcgctc 120
gatctgggat ttcagtttgg ggacaccggg cgtgaactca tgatgcagat tcagccggggg 180
cagcaatatc ccggcatgtt gcgcacgctg ctgcctcgtc gttatcagca ggcggcagag 240
tgcgatggct gccatctgtg cctgaacggc agcgatgtat tgatcctctg gtggccgctg 300
ccgtcggatc ccggcagtta tccgcaggtg atcgaacgtt tgtttgaact ggcggggaatg 360
acgttgccgt cgctatccat agcaccgacg gcgcgtccgc agacagggaa cggacgcgcc 420
cgatcattaa gataaaggcg gcttttttta ttgcaaacg gtaacgggtga ggaaccgttt 480
caccgtcggc gtcactcagt aacaagtatc catcatgatg cctacatcgg gatcggcgctg 540
ggcatccgtt gcagatactt ttgcgaacac ctgacatgaa tgaggaaacg aaattatgca 600
aattacgatc aaagcgcaca tcggcggtga tttgggcgtc tccgggtctgg ggctgggtgc 660
tcagggactg aaaggactga attccgcggc ttcctcgtg ggttccagcg tggataaact 720
gagcagcacc atcgataagt tgacctccgc gctgacttcg atgatgtttg gcggcgcgct 780
ggcgcgaggg ctgggcgcca gctcgaaggg gctggggatg agcaatcaac tgggccagtc 840
tttcggcaat ggcgcgagg gtgogagcaa cctgctatcc gtaccgaaat ccggcgcgca 900
tgcgttgtca aaaaatgtttg ataaagcgct ggacgatctg ctgggtcatg acaccgtgac 960
caagctgact aaccagagca accaactggc taattcaatg ctgaacgcca gccagatgac 1020
ccagggtaat atgaatgcgt tcggcagcgg tgtgaacaac gcaactgtcgt ccattctcgg 1080
caacggtctc ggccagtcga tgagtggctt ctctcagcct tctctggggg caggcggtct 1140
gcagggcctg agcggcgcggt gtgcattcaa ccagttgggt aatgccatcg gcatgggcgt 1200
ggggcagaat gctgcgctga gtgcgttgag taacgtcagc acccacgtag acggtaacaa 1260
ccgccacttt gtagataaag aagatcgcg catggcgaaa gagatcgggc agtttatgga 1320
tcagtatccg gaaatattcg gtaaaccgga ataccagaaa gatggctgga gttcgccgaa 1380
gacggacgac aaatcctggg ctaaagcgct gagtaaaccg gatgatgacg gtatgaccgg 1440
cgccagcatg gacaaattcc gtcaggcgat gggatgatc aaaagcgcgg tggcggtga 1500
taccggcaat accaacctga acctgcgtgg cgcgggcggt gcatcgtggt gtatcgatgc 1560
ggctgtcgtc ggcgataaaa tagccaacat gtcgctgggt aagctggcca acgcctgata 1620
atctgtgctg gcctgataaa gcggaaacga aaaaagagac gggaagcct gtctcttttc 1680
ttattatgcg gtttatgcgg ttacctggac cggttaatca tcgtcatcga tctggtacaa 1740
acgcacattt tcccgttcat tcgcgtcgtt acgcgccaca atcgcgatgg catcttcctc 1800
gtcgtcaga ttgcgcggct gatggggaac gccgggtgga atatatagaa actcgccggc 1860
cagatggaga cagctctcgt ataaatctgt gccgtaacgt gtttctatcc gcccttttag 1920
cagatagatt gcggtttcgt aatcaacatg gtaatgcggt tccgcctgtg cgccggccgg 1980
gatcaccaca atattcatag aaagctgtct tgcacctacc gtatcgcggg agataccgac 2040
aaaatagggc agtttttgcg tggtatccgt ggggtgttcc ggctgacaa tcttgagttg 2100
gttcgtcatc atctttctcc atctgggcga cctgatcgtt t 2141

<210> 3

<211> 403

<212> PRT

<213> *Erwinia amylovora*

<400> 3

Met Ser Leu Asn Thr Ser Gly Leu Gly Ala Ser Thr Met Gln Ile Ser

1	5	10	15
Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln	20	25	30
Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Gly Asn	35	40	45
Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met	50	55	60
Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu	65	70	75
Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu	85	90	95
Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr	100	105	110
Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro	115	120	125
Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser	130	135	140
Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln	145	150	155
Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly	165	170	175
Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu	180	185	190
Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly	195	200	205
Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly	210	215	220
Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu	225	230	235
Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln	245	250	255
Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln			

260	265	270
Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe		
275	280	285
Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met		
290	295	300
Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro		
305	310	315
Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser		
325	330	335
Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn		
340	345	350
Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn		
355	360	365
Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp		
370	375	380
Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu		
385	390	395
Gly Ala Ala		

<210> 4
 <211> 1288
 <212> DNA
 <213> Erwinia amylovora

<400> 4
 aagcttcggc atggcacggt tgaccgttgg gtcggcaggg tacgtttgaa ttattcataa 60
 gaggaatacgt ttatgagtct gaatacaagt gggctgggag cgtcaacgat gcaaatttct 120
 atcggcggtg cgggcggaaa taacgggttg ctgggtacca gtcgccagaa tgctgggttg 180
 ggtggcaatt ctgcactggg gctgggcggc ggtaatcaaa atgataccgt caatcagctg 240
 gctggcttac tcaccggcat gatgatgat atgagcatga tgggcggtgg tgggctgatg 300
 ggcggtggct taggcggtgg cttaggtaat ggcttgggtg gctcaggtgg cctgggcgaa 360
 ggactgtcga acgcgctgaa cgatatgtta ggcggttcgc tgaacacgct gggctcgaaa 420
 ggcggcaaca ataccacttc aacaacaaat tccccgctgg accaggcgct ggggtattaac 480
 tcaacgtccc aaaacgacga ttccacctcc ggcacagatt ccacctcaga ctccagcgac 540
 ccgatgcagc agctgctgaa gatgttcagc gagataatgc aaagcctgtt tgggtgatggg 600
 caagatggca ccaggggcag ttcctctggg ggcaagcagc cgaccgaagg cgagcagaac 660
 gcctataaaa aaggagtcac tgatgcgctg tcgggcctga tgggtaatgg tctgagccag 720

```
ctccttggca acgggggact gggaggtggt cagggcggta atgctggcac gggctctgac 780
ggttcgtcgc tgggcggcaa agggctgcaa aacctgagcg ggccgggtgga ctaccagcag 840
ttaggtaacg ccgtgggtac cggtatcggc atgaaagcgg gcattcaggc gctgaatgat 900
atcggtagcg acaggcacag ttcaaccctg tctttcgtca ataaaggcga tcgggcgatg 960
gcgaagggaa tcggtcagtt catggaccag tatcctgagg tgtttggcaa gccgcagtac 1020
cagaaaggcc cgggtcagga ggtgaaaacc gatgacaaat catgggcaaa agcactgagc 1080
aagccagatg acgacggaat gacaccagcc agtatggagc agttcaaca agccaagggc 1140
atgatcaaaa ggcccatggc gggtgatacc ggcaacggca acctgcaggc acgcggtgcc 1200
ggtggttctt cgctgggtat tgatgccatg atggccgggtg atgccattaa caatatggca 1260
cttggcaagc tgggcgcggc ttaagctt 1288
```

<210> 5
 <211> 1344
 <212> DNA
 <213> *Erwinia amylovora*

```
<400> 5
atgtcaattc ttacgcttaa caacaatacc tgcctctcgc cgggtctggt ccagtcgggg 60
ggggacaacg ggcttggtgg tcataatgca aattctgcgt tggggcaaca acccatcgat 120
cggcaaacca ttgagcaaat ggctcaatta ttggcggaac tgttaaagtc actgctatcg 180
ccacaatcag gtaatgcggc aaccggagcc ggtggcaatg accagaactac aggagttggt 240
aacgctggcg gcctgaacgg acgaaaaggc acagcaggaa ccaactccgca gtctgacagt 300
cagaacatgc tgagtggatg gggcaacaac gggctggatc aggccatcac gccgatggc 360
cagggcggcg ggcagatcgg cgataatcct ttactgaaag ccactgctga gcttattgca 420
cgcatgatgg acggccaaa cgatcagttt ggccaacctg gtacgggcaa caacagtgcc 480
tcttcgggta cttcttcacg tggcggttcc ctttttaacg atctatcagg ggggaaggcc 540
ccttcgggca actcccttc cggcaactac tctcccgta gtaccttctc acccccatcc 600
acgccaacgt cccctacctc accgcttgat ttcccttctt cccccaccaa agcagccggg 660
ggcagcacgc cggtaaccga tcatcctgac cctgttggtg gcgcgggcat cggggccgga 720
aattcgggtg ccttcaccag cgcggcgct aatcagacgg tgctgcatga caccattacc 780
gtgaaagcgg gtcaggtggt tgatggcaaa ggacaaacct tcaccgccgg ttcagaatta 840
ggcgatggcg gccagtctga aaaccagaaa ccgctgttta tactggaaga cggtgccagc 900
ctgaaaaacg tcaccatggg cgacgacggg gcggatggta ttcattctta cggtgatgcc 960
aaaatagaca atctgcacgt caccaacgtg ggtgaggacg cgattaccgt taagccaaac 1020
agcgcgggca aaaaatccca cgttgaaatc actaacagtt ccttcgagca cgctctgac 1080
aagatcctgc agctgaatgc cgatactaac ctgagcggtt acaacgtgaa ggccaaagac 1140
tttggtactt ttgtacgcac taacggcggt caacagggtg actgggatct gaatctgagc 1200
catatcagcg cagaagacgg taagttctcg ttcggttaaaa gcgatagcga ggggctaaac 1260
gtcaatacca gtgatctctc actgggtgat gttgaaaacc actacaaagt gccgatgtcc 1320
gccaacctga aggtggctga atga 1344
```

<210> 6
 <211> 447
 <212> PRT
 <213> *Erwinia amylovora*

09079249 064304

<400> 6

Met Ser Ile Leu Thr Leu Asn Asn Asn Thr Ser Ser Ser Pro Gly Leu
1 5 10 15

Phe Gln Ser Gly Gly Asp Asn Gly Leu Gly Gly His Asn Ala Asn Ser
20 25 30

Ala Leu Gly Gln Gln Pro Ile Asp Arg Gln Thr Ile Glu Gln Met Ala
35 40 45

Gln Leu Leu Ala Glu Leu Leu Lys Ser Leu Leu Ser Pro Gln Ser Gly
50 55 60

Asn Ala Ala Thr Gly Ala Gly Gly Asn Asp Gln Thr Thr Gly Val Gly
65 70 75 80

Asn Ala Gly Gly Leu Asn Gly Arg Lys Gly Thr Ala Gly Thr Thr Pro
85 90 95

Gln Ser Asp Ser Gln Asn Met Leu Ser Glu Met Gly Asn Asn Gly Leu
100 105 110

Asp Gln Ala Ile Thr Pro Asp Gly Gln Gly Gly Gly Gln Ile Gly Asp
115 120 125

Asn Pro Leu Leu Lys Ala Met Leu Lys Leu Ile Ala Arg Met Met Asp
130 135 140

Gly Gln Ser Asp Gln Phe Gly Gln Pro Gly Thr Gly Asn Asn Ser Ala
145 150 155 160

Ser Ser Gly Thr Ser Ser Ser Gly Gly Ser Pro Phe Asn Asp Leu Ser
165 170 175

Gly Gly Lys Ala Pro Ser Gly Asn Ser Pro Ser Gly Asn Tyr Ser Pro
180 185 190

Val Ser Thr Phe Ser Pro Pro Ser Thr Pro Thr Ser Pro Thr Ser Pro
195 200 205

Leu Asp Phe Pro Ser Ser Pro Thr Lys Ala Ala Gly Gly Ser Thr Pro
210 215 220

Val Thr Asp His Pro Asp Pro Val Gly Ser Ala Gly Ile Gly Ala Gly
225 230 235 240

Asn Ser Val Ala Phe Thr Ser Ala Gly Ala Asn Gln Thr Val Leu His
245 250 255

Asp Thr Ile Thr Val Lys Ala Gly Gln Val Phe Asp Gly Lys Gly Gln
260 265 270

Thr Phe Thr Ala Gly Ser Glu Leu Gly Asp Gly Gly Gln Ser Glu Asn
275 280 285

Gln Lys Pro Leu Phe Ile Leu Glu Asp Gly Ala Ser Leu Lys Asn Val
290 295 300

Thr Met Gly Asp Asp Gly Ala Asp Gly Ile His Leu Tyr Gly Asp Ala
305 310 315 320

Lys Ile Asp Asn Leu His Val Thr Asn Val Gly Glu Asp Ala Ile Thr
325 330 335

Val Lys Pro Asn Ser Ala Gly Lys Lys Ser His Val Glu Ile Thr Asn
340 345 350

Ser Ser Phe Glu His Ala Ser Asp Lys Ile Leu Gln Leu Asn Ala Asp
355 360 365

Thr Asn Leu Ser Val Asp Asn Val Lys Ala Lys Asp Phe Gly Thr Phe
370 375 380

Val	Arg	Thr	Asn	Gly	Gly	Gln	Gln	Gly	Asn	Trp	Asp	Leu	Asn	Leu	Ser
385					390					395					400

His Ile Ser Ala Glu Asp Gly Lys Phe Ser Phe Val Lys Ser Asp Ser
405 410 415

Glu Gly Leu Asn Val Asn Thr Ser Asp Ile Ser Leu Gly Asp Val Glu
420 425 430

Asn His Tyr Lys Val Pro Met Ser Ala Asn Leu Lys Val Ala Glu
435 440 445

 $\langle 210 \rangle$ 7

<211> 5517

<212> DNA

<213> Erwinia amylovora

<400> 7

atggaattaa	aatcactggg	aactgaacac	aaggcggcag	tacacacagc	ggcgcaaac	60
cctgtggggc	atgggtgttc	cttacagcag	ggcagcagca	gcagcagccc	gcaaaatgcc	120
gctgcatcat	tggcggcaga	aggcaaaaat	cgtgggaaaa	tgccgagaat	tcaccagcca	180
tctactgcgg	ctgatggtat	cagcgcctgt	caccagcaaa	agaaatcctt	cagtctcagg	240


```

ggctgttttg ggacgaaaaa attttccaga tcggcaccgc agggccagcc aggtaccacc 300
cacagcaaag gggcaacatt gcgcgatctg ctggcgcggg acgacggcga aacgcagcat 360
gaggcgcccg cgccagatgc ggcgcgtttg acccgttcgg gcggcgctcaa acgccgcaat 420
atggacgaca tggcggggcg gccaatggtg aaaggtggca gcggcggaaga taaggtacca 480
acgcagcaaa aacggcatca gctgaacaat tttggccaga tgcgccaaac gatgttgagc 540
aaaatggctc acccggttc agccaacgcc ggcgatcgcc tgcagcattc accgccgcac 600
atcccggtta gccaccacga aatcaaggaa gaaccggttg gctccaccag caaggcaaca 660
acggcccacg cagacagagt ggaaatcgct caggaagatg acgacagcga attccagcaa 720
ctgcatcaac agcggctggc gcgcgaacgg gaaaaatccac cgcagccgcc caaactcggc 780
gttgccacac cgattagcgc caggtttcag cccaaactga ctgcgggttg ggaaagcgtc 840
cttgagggga cagataccac gcagtcaccc cttaagccgc aatcaatgct gaaaggaagt 900
ggagccgggg taacgccgct ggcggtaacg ctggataaag gcaagttgca gctggcaccg 960
gataatccac ccgcgctcaa tacgttggtg aagcagacat tgggtaaaga caccagcac 1020
tatctggcgc accatgccag cagcgacggt agccagcatc tgctgctgga caacaaaggc 1080
cacctgtttg atatcaaaag caccgccacc agctatagcg tgctgcacaa cagccacccc 1140
ggtgagataa agggcaagct ggcgcaggcg ggtactggct ccgtcagcgt agacggtaaa 1200
agcggcaaga tctcgtggg gagcgggtacg caaagtcaca acaaaacaat gctaagccaa 1260
ccgggggaag cgcaccgttc cttattaacc ggcatttggc agcatcctgc tggcgcagcg 1320
cggccgcagg gcgagtcaat ccgcctgcat gacgacaaaa ttcataatcct gcacccggag 1380
ctgggcgtat ggcaatctgc ggataaagat acccacagcc agctgtctcg ccaggcagac 1440
ggtaagctct atgcgtgaa agacaaccgt accctgcaaa acctctcga taataaatcc 1500
tcagaaaagc tggtcgataa aatcaaatcg tattccgttg atcagcgggg gcaggtggcg 1560
atcctgacgg atactcccg ccgccataag atgagtatta tgccctcgct ggatgcttcc 1620
ccggagagcc atatttcct cagcctgcat tttgccgatg ccaccaggg gttattgcac 1680
gggaagtccg agcttgaggc acaatctgtc gcgatcagcc atgggcgact ggttgtggcc 1740
gatagcgaag gcaagctgtt tagcgccgcc attccgaagc aaggggatgg aaacgaactg 1800
aaaatgaaag ccatgcctca gcatgcgtc gatgaacatt ttggtcatga ccaccagatt 1860
tctggatttt tccatgacga ccacggccag cttaatgcgc tggtgaaaaa taacttcagg 1920
cagcagcatg cctgcccggt gggtaacgat catcagtttc accccggctg gaacctgact 1980
gatgcgctgg ttatcgacaa tcagctgggg ctgcatcata ccaatcctga accgcatgag 2040
attcttgata tggggcattht aggcagcctg gcgttacagg agggcaagct tcaactattht 2100
gaccagctga ccaaagggtg gactggcgcg gagtcagatt gtaagcagct gaaaaaaggc 2160
ctggatggag cagcttatct actgaaagac ggtgaagtga aacgcctgaa tattaatcag 2220
agcacctcct ctatcaagca cggaacggaa aacgtthttt cgctgccgca tgtgcgcaat 2280
aaaccggagc cgggagatgc cctgcaaggg ctgaataaag acgataaggc ccaggccatg 2340
gcggtgattg gggtaaataa atacctggcg ctgacggaaa aaggggacat tcgctccttc 2400
cagataaaaac ccgpcacca gcagttggag cgcccgccac aaactctcag ccgcgaagg 2460
atcagcggcg aactgaaaga cattcatgtc gaccacaagc agaacctgta tgcttgacc 2520
cacgaggag aggtgtttca tcagccgctg gaagcctggc agaatggtgc cgaaagcagc 2580
agctggcaca aactggcggt gccacagagt gaaagtaagc taaaaagtct ggacatgagc 2640
catgagcaca aaccgattgc cacctttgaa gacggtagcc agcatcagct gaaggctggc 2700
ggctggcacg cctatgcggc acctgaacgc gggccgctgg cgggtgggtac cagcggttca 2760
caaaccgtct ttaaccgact aatgcagggg gtgaaaggca aggtgatccc aggcagcggg 2820
ttgacggtta agctctcgcc tcagacgggg ggaatgaccg gcgccgaagg gcgcaaggtc 2880
agcagtaaat tttccgaaag gatccgcgcc tatgcgttca acccaacaat gtccacgccg 2940
cgaccgatta aaaatgctgc ttatgccaca cagcacggct ggcagggggc tgaggggttg 3000
aagccgttg acgagatgca gggagcgctg attaaacaac tggatgcgca taacgttcgt 3060
cataacgcgc cacagccaga tttgcagagc aaactggaaa ctctggattt aggcgaacat 3120

```

ggcgagagaat	tgcttaacga	catgaagcgc	ttccgcgacg	aactggagca	gagtgaaccc	3180
ggttcggtga	ccgttttagg	tcaacatcag	ggagtgctaa	aaagcaacgg	tgaatcaat	3240
agcgaattta	agccatcgcc	cggcaaggcg	ttggtccaga	gctttaacgt	caatcgctct	3300
ggtcagggatc	taagcaagtc	actgcaacag	gcagtacatg	ccacgcgcgc	atccgcagag	3360
agtaaactgc	aatccatgct	ggggcacttt	gtcagtgccg	gggtggatat	gagtcacag	3420
aagggcgaga	tcccgtggg	ccgccagcgc	gatccgaatg	ataaaaccgc	actgaccaa	3480
tcgcgtttta	ttttagatac	cgtgaccatc	ggtgaactgc	atgaactggc	cgataaggcg	3540
aaactggtat	ctgaccataa	accgatgcc	gatcagataa	aacagctgcg	ccagcagttc	3600
gatacgtgc	gtgaaaagcg	gtatgagagc	aatccggtga	agcattacac	cgatatgggc	3660
ttcacccata	ataaggcgct	ggaagcaaac	tatgatgcgg	tcaaagcctt	tatcaatgcc	3720
tttaagaaaag	agcaccacgg	cgtcaatctg	accacgcgta	ccgtactgga	atcacagggc	3780
agtgcggagc	tggcgaagaa	gctcaagaat	acgctgttgt	ccttggaacg	tggtgaaagt	3840
atgagcttca	gccggtcata	tggcgggggc	gtcagcactg	tctttgtgcc	tacccttagc	3900
aagaaggtgc	cagttccggg	gatcccgga	gcggcgcata	cgctggatcg	cgctataaac	3960
ctgagcttca	gtcgtaccag	cggcggtatg	aacgtcagtt	ttggccgcga	cggcggggtg	4020
agtggtaaca	tcatggtcgc	taccggccat	gatgtgatgc	cctatatgac	cggtaagaaa	4080
accagtgcag	gtaacgccag	tgactggttg	agcgcaaaac	ataaaatcag	cccggaactg	4140
cgtatcggcg	ctgctgtgag	tggcacctcg	caaggaaacg	tacaaaacag	cctgaagttt	4200
aagctgacag	aggatgagct	gcctggcttt	atccatggct	tgacgcagtg	cacgttgacc	4260
ccggcagaac	tgttgcaaaa	ggggatcgaa	catcagatga	agcagggcag	caaaactgacg	4320
tttagcgctg	atacctcggc	aaatctggat	ctgcgtgccg	gtatcaatct	gaacgaagac	4380
ggcagtaaac	caaatggtgt	cactgcccgt	gtttctgccg	ggctaagtgc	atcggcaaac	4440
ctggccgcgc	gctcgcgta	acgcagcacc	acctctggcc	agtttggcag	cacgaactcg	4500
gccagcaata	accgcccaac	cttctcaac	ggggctcgcg	cggtgctaa	cctgacggct	4560
gctttagggg	ttgccatttc	atctacgat	gaagggaaac	cggtcgggat	cttcccggca	4620
tttaacctga	ccaatgtttc	ggcagcgctg	gcgctggata	accgtacctc	acagagtatc	4680
agcctggaat	tgaagcgcg	ggagccggtg	accagcaacg	atatcagcga	gttgacctcc	4740
acgctgggaa	aacactttta	ggatagcgcc	acaacgaaga	tgttgccgc	tctcaaagag	4800
ttagatgacg	ctaagccgcg	tgaacaactg	catattttac	agcagcattt	cagtgcacaa	4860
gatgtcgctg	gtgatgaacg	ctacgaggcg	gtgcgcaacc	tgaaaaaact	ggtgatagct	4920
caacagggtg	cggacagcca	cagcatggaa	ttaggatctg	ccagtcacag	cacgacctac	4980
aataatctgt	cgagaataaa	taatgacggc	attgtcgagc	tgtacacaa	acatttcgat	5040
gcggcattac	cagcaagcag	tgccaaacgt	cttggtgaaa	tgatgaataa	cgatccggca	5100
ctgaaagata	ttattaagca	gctgcaaagt	acgccgttca	gcagcgccag	cgtgtcgatg	5160
gagctgaaag	atggtctgcg	tgagcagacg	gaaaaagcaa	tactggacgg	taaggtcggt	5220
cgtgaagaag	tgggagtact	tttcagggat	cgtaacaact	tgcgtgttaa	atcggtcagc	5280
gtcagtcagt	ccgtcagcaa	aagcgaaggc	ttcaataccc	cagcgtgttt	actggggacg	5340
agcaacagcg	ctgctatgag	catggagcgc	aacatcgga	ccattaattt	taaatacggc	5400
caggatcaga	acaccccaag	gcgatttacc	ctggagggtg	gaatagctca	ggctaataccg	5460
caggtcgcat	ctgcgcttac	tgatttgaag	aaggaagggc	tggaaatgaa	gagctaa	5517

<210> 8

<211> 1838

<212> PRT

<213> Erwinia amylovora

<400> 8

Met Glu Leu Lys Ser Leu Gly Thr Glu His Lys Ala Ala Val His Thr
 1 5 10 15
 Ala Ala His Asn Pro Val Gly His Gly Val Ala Leu Gln Gln Gly Ser
 20 25 30
 Ser Ser Ser Ser Pro Gln Asn Ala Ala Ala Ser Leu Ala Ala Glu Gly
 35 40 45
 Lys Asn Arg Gly Lys Met Pro Arg Ile His Gln Pro Ser Thr Ala Ala
 50 55 60
 Asp Gly Ile Ser Ala Ala His Gln Gln Lys Lys Ser Phe Ser Leu Arg
 65 70 75 80
 Gly Cys Leu Gly Thr Lys Lys Phe Ser Arg Ser Ala Pro Gln Gly Gln
 85 90 95
 Pro Gly Thr Thr His Ser Lys Gly Ala Thr Leu Arg Asp Leu Leu Ala
 100 105 110
 Arg Asp Asp Gly Glu Thr Gln His Glu Ala Ala Ala Pro Asp Ala Ala
 115 120 125
 Arg Leu Thr Arg Ser Gly Gly Val Lys Arg Arg Asn Met Asp Asp Met
 130 135 140
 Ala Gly Arg Pro Met Val Lys Gly Gly Ser Gly Glu Asp Lys Val Pro
 145 150 155 160
 Thr Gln Gln Lys Arg His Gln Leu Asn Asn Phe Gly Gln Met Arg Gln
 165 170 175
 Thr Met Leu Ser Lys Met Ala His Pro Ala Ser Ala Asn Ala Gly Asp
 180 185 190
 Arg Leu Gln His Ser Pro Pro His Ile Pro Gly Ser His His Glu Ile
 195 200 205
 Lys Glu Glu Pro Val Gly Ser Thr Ser Lys Ala Thr Thr Ala His Ala
 210 215 220
 Asp Arg Val Glu Ile Ala Gln Glu Asp Asp Asp Ser Glu Phe Gln Gln
 225 230 235 240
 Leu His Gln Gln Arg Leu Ala Arg Glu Arg Glu Asn Pro Pro Gln Pro
 245 250 255

Pro	Lys	Leu	Gly	Val	Ala	Thr	Pro	Ile	Ser	Ala	Arg	Phe	Gln	Pro	Lys	260	265	270
Leu	Thr	Ala	Val	Ala	Glu	Ser	Val	Leu	Glu	Gly	Thr	Asp	Thr	Thr	Gln	275	280	285
Ser	Pro	Leu	Lys	Pro	Gln	Ser	Met	Leu	Lys	Gly	Ser	Gly	Ala	Gly	Val	290	295	300
Thr	Pro	Leu	Ala	Val	Thr	Leu	Asp	Lys	Gly	Lys	Leu	Gln	Leu	Ala	Pro	305	310	315
Asp	Asn	Pro	Pro	Ala	Leu	Asn	Thr	Leu	Leu	Lys	Gln	Thr	Leu	Gly	Lys	325	330	335
Asp	Thr	Gln	His	Tyr	Leu	Ala	His	His	Ala	Ser	Ser	Asp	Gly	Ser	Gln	340	345	350
His	Leu	Leu	Leu	Asp	Asn	Lys	Gly	His	Leu	Phe	Asp	Ile	Lys	Ser	Thr	355	360	365
Ala	Thr	Ser	Tyr	Ser	Val	Leu	His	Asn	Ser	His	Pro	Gly	Glu	Ile	Lys	370	375	380
Gly	Lys	Leu	Ala	Gln	Ala	Gly	Thr	Gly	Ser	Val	Ser	Val	Asp	Gly	Lys	385	390	395
Ser	Gly	Lys	Ile	Ser	Leu	Gly	Ser	Gly	Thr	Gln	Ser	His	Asn	Lys	Thr	405	410	415
Met	Leu	Ser	Gln	Pro	Gly	Glu	Ala	His	Arg	Ser	Leu	Leu	Thr	Gly	Ile	420	425	430
Trp	Gln	His	Pro	Ala	Gly	Ala	Ala	Arg	Pro	Gln	Gly	Glu	Ser	Ile	Arg	435	440	445
Leu	His	Asp	Asp	Lys	Ile	His	Ile	Leu	His	Pro	Glu	Leu	Gly	Val	Trp	450	455	460
Gln	Ser	Ala	Asp	Lys	Asp	Thr	His	Ser	Gln	Leu	Ser	Arg	Gln	Ala	Asp	465	470	475
Gly	Lys	Leu	Tyr	Ala	Leu	Lys	Asp	Asn	Arg	Thr	Leu	Gln	Asn	Leu	Ser	485	490	495
Asp	Asn	Lys	Ser	Ser	Glu	Lys	Leu	Val	Asp	Lys	Ile	Lys	Ser	Tyr	Ser	500	505	510

09079248-061304

Val	Asp	Gln	Arg	Gly	Gln	Val	Ala	Ile	Leu	Thr	Asp	Thr	Pro	Gly	Arg	515	520	525	
His	Lys	Met	Ser	Ile	Met	Pro	Ser	Leu	Asp	Ala	Ser	Pro	Glu	Ser	His	530	535	540	
Ile	Ser	Leu	Ser	Leu	His	Phe	Ala	Asp	Ala	His	Gln	Gly	Leu	Leu	His	545	550	555	560
Gly	Lys	Ser	Glu	Leu	Glu	Ala	Gln	Ser	Val	Ala	Ile	Ser	His	Gly	Arg	565	570	575	
Leu	Val	Val	Ala	Asp	Ser	Glu	Gly	Lys	Leu	Phe	Ser	Ala	Ala	Ile	Pro	580	585	590	
Lys	Gln	Gly	Asp	Gly	Asn	Glu	Leu	Lys	Met	Lys	Ala	Met	Pro	Gln	His	595	600	605	
Ala	Leu	Asp	Glu	His	Phe	Gly	His	Asp	His	Gln	Ile	Ser	Gly	Phe	Phe	610	615	620	
His	Asp	Asp	His	Gly	Gln	Leu	Asn	Ala	Leu	Val	Lys	Asn	Asn	Phe	Arg	625	630	635	640
Gln	Gln	His	Ala	Cys	Pro	Leu	Gly	Asn	Asp	His	Gln	Phe	His	Pro	Gly	645	650	655	
Trp	Asn	Leu	Thr	Asp	Ala	Leu	Val	Ile	Asp	Asn	Gln	Leu	Gly	Leu	His	660	665	670	
His	Thr	Asn	Pro	Glu	Pro	His	Glu	Ile	Leu	Asp	Met	Gly	His	Leu	Gly	675	680	685	
Ser	Leu	Ala	Leu	Gln	Glu	Gly	Lys	Leu	His	Tyr	Phe	Asp	Gln	Leu	Thr	690	695	700	
Lys	Gly	Trp	Thr	Gly	Ala	Glu	Ser	Asp	Cys	Lys	Gln	Leu	Lys	Lys	Gly	705	710	715	720
Leu	Asp	Gly	Ala	Ala	Tyr	Leu	Leu	Lys	Asp	Gly	Glu	Val	Lys	Arg	Leu	725	730	735	
Asn	Ile	Asn	Gln	Ser	Thr	Ser	Ser	Ile	Lys	His	Gly	Thr	Glu	Asn	Val	740	745	750	
Phe	Ser	Leu	Pro	His	Val	Arg	Asn	Lys	Pro	Glu	Pro	Gly	Asp	Ala	Leu	755	760	765	

Gln	Gly	Leu	Asn	Lys	Asp	Asp	Lys	Ala	Gln	Ala	Met	Ala	Val	Ile	Gly	770	775	780	
Val	Asn	Lys	Tyr	Leu	Ala	Leu	Thr	Glu	Lys	Gly	Asp	Ile	Arg	Ser	Phe	785	790	795	800
Gln	Ile	Lys	Pro	Gly	Thr	Gln	Gln	Leu	Glu	Arg	Pro	Ala	Gln	Thr	Leu	805	810	815	
Ser	Arg	Glu	Gly	Ile	Ser	Gly	Glu	Leu	Lys	Asp	Ile	His	Val	Asp	His	820	825	830	
Lys	Gln	Asn	Leu	Tyr	Ala	Leu	Thr	His	Glu	Gly	Glu	Val	Phe	His	Gln	835	840	845	
Pro	Arg	Glu	Ala	Trp	Gln	Asn	Gly	Ala	Glu	Ser	Ser	Ser	Trp	His	Lys	850	855	860	
Leu	Ala	Leu	Pro	Gln	Ser	Glu	Ser	Lys	Leu	Lys	Ser	Leu	Asp	Met	Ser	865	870	875	880
His	Glu	His	Lys	Pro	Ile	Ala	Thr	Phe	Glu	Asp	Gly	Ser	Gln	His	Gln	885	890	895	
Leu	Lys	Ala	Gly	Gly	Trp	His	Ala	Tyr	Ala	Ala	Pro	Glu	Arg	Gly	Pro	900	905	910	
Leu	Ala	Val	Gly	Thr	Ser	Gly	Ser	Gln	Thr	Val	Phe	Asn	Arg	Leu	Met	915	920	925	
Gln	Gly	Val	Lys	Gly	Lys	Val	Ile	Pro	Gly	Ser	Gly	Leu	Thr	Val	Lys	930	935	940	
Leu	Ser	Ala	Gln	Thr	Gly	Gly	Met	Thr	Gly	Ala	Glu	Gly	Arg	Lys	Val	945	950	955	960
Ser	Ser	Lys	Phe	Ser	Glu	Arg	Ile	Arg	Ala	Tyr	Ala	Phe	Asn	Pro	Thr	965	970	975	
Met	Ser	Thr	Pro	Arg	Pro	Ile	Lys	Asn	Ala	Ala	Tyr	Ala	Thr	Gln	His	980	985	990	
Gly	Trp	Gln	Gly	Arg	Glu	Gly	Leu	Lys	Pro	Leu	Tyr	Glu	Met	Gln	Gly	995	1000	1005	
Ala	Leu	Ile	Lys	Gln	Leu	Asp	Ala	His	Asn	Val	Arg	His	Asn	Ala	Pro	1010	1015	1020	

[illegible]

Met	Ser	Phe	Ser	Arg	Ser	Tyr	Gly	Gly	Gly	Val	Ser	Thr	Val	Phe	Val	1285	1290	1295	
Pro	Thr	Leu	Ser	Lys	Lys	Val	Pro	Val	Pro	Val	Ile	Pro	Gly	Ala	Gly	1300	1305	1310	
Ile	Thr	Leu	Asp	Arg	Ala	Tyr	Asn	Leu	Ser	Phe	Ser	Arg	Thr	Ser	Gly	1315	1320	1325	
Gly	Leu	Asn	Val	Ser	Phe	Gly	Arg	Asp	Gly	Gly	Val	Ser	Gly	Asn	Ile	1330	1335	1340	
Met	Val	Ala	Thr	Gly	His	Asp	Val	Met	Pro	Tyr	Met	Thr	Gly	Lys	Lys	1345	1350	1355	1360
Thr	Ser	Ala	Gly	Asn	Ala	Ser	Asp	Trp	Leu	Ser	Ala	Lys	His	Lys	Ile	1365	1370	1375	
Ser	Pro	Asp	Leu	Arg	Ile	Gly	Ala	Ala	Val	Ser	Gly	Thr	Leu	Gln	Gly	1380	1385	1390	
Thr	Leu	Gln	Asn	Ser	Leu	Lys	Phe	Lys	Leu	Thr	Glu	Asp	Glu	Leu	Pro	1395	1400	1405	
Gly	Phe	Ile	His	Gly	Leu	Thr	His	Gly	Thr	Leu	Thr	Pro	Ala	Glu	Leu	1410	1415	1420	
Leu	Gln	Lys	Gly	Ile	Glu	His	Gln	Met	Lys	Gln	Gly	Ser	Lys	Leu	Thr	1425	1430	1435	1440
Phe	Ser	Val	Asp	Thr	Ser	Ala	Asn	Leu	Asp	Leu	Arg	Ala	Gly	Ile	Asn	1445	1450	1455	
Leu	Asn	Glu	Asp	Gly	Ser	Lys	Pro	Asn	Gly	Val	Thr	Ala	Arg	Val	Ser	1460	1465	1470	
Ala	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Leu	Ala	Ala	Gly	Ser	Arg	Glu	Arg	1475	1480	1485	
Ser	Thr	Thr	Ser	Gly	Gln	Phe	Gly	Ser	Thr	Thr	Ser	Ala	Ser	Asn	Asn	1490	1495	1500	
Arg	Pro	Thr	Phe	Leu	Asn	Gly	Val	Gly	Ala	Gly	Ala	Asn	Leu	Thr	Ala	1505	1510	1515	1520
Ala	Leu	Gly	Val	Ala	His	Ser	Ser	Thr	His	Glu	Gly	Lys	Pro	Val	Gly	1525	1530	1535	

Ile Phe Pro Ala Phe Thr Ser Thr Asn Val Ser Ala Ala Leu Ala Leu	1540	1545	1550
Asp Asn Arg Thr Ser Gln Ser Ile Ser Leu Glu Leu Lys Arg Ala Glu	1555	1560	1565
Pro Val Thr Ser Asn Asp Ile Ser Glu Leu Thr Ser Thr Leu Gly Lys	1570	1575	1580
His Phe Lys Asp Ser Ala Thr Thr Lys Met Leu Ala Ala Leu Lys Glu	1585	1590	1595
Leu Asp Asp Ala Lys Pro Ala Glu Gln Leu His Ile Leu Gln Gln His	1605	1610	1615
Phe Ser Ala Lys Asp Val Val Gly Asp Glu Arg Tyr Glu Ala Val Arg	1620	1625	1630
Asn Leu Lys Lys Leu Val Ile Arg Gln Gln Ala Ala Asp Ser His Ser	1635	1640	1645
Met Glu Leu Gly Ser Ala Ser His Ser Thr Thr Tyr Asn Asn Leu Ser	1650	1655	1660
Arg Ile Asn Asn Asp Gly Ile Val Glu Leu Leu His Lys His Phe Asp	1665	1670	1675
Ala Ala Leu Pro Ala Ser Ser Ala Lys Arg Leu Gly Glu Met Met Asn	1685	1690	1695
Asn Asp Pro Ala Leu Lys Asp Ile Ile Lys Gln Leu Gln Ser Thr Pro	1700	1705	1710
Phe Ser Ser Ala Ser Val Ser Met Glu Leu Lys Asp Gly Leu Arg Glu	1715	1720	1725
Gln Thr Glu Lys Ala Ile Leu Asp Gly Lys Val Gly Arg Glu Glu Val	1730	1735	1740
Gly Val Leu Phe Gln Asp Arg Asn Asn Leu Arg Val Lys Ser Val Ser	1745	1750	1755
Val Ser Gln Ser Val Ser Lys Ser Glu Gly Phe Asn Thr Pro Ala Leu	1765	1770	1775
Leu Leu Gly Thr Ser Asn Ser Ala Ala Met Ser Met Glu Arg Asn Ile	1780	1785	1790

Gly Thr Ile Asn Phe Lys Tyr Gly Gln Asp Gln Asn Thr Pro Arg Arg
1795 1800 1805

Phe Thr Leu Glu Gly Gly Ile Ala Gln Ala Asn Pro Gln Val Ala Ser
1810 1815 1820

Ala Leu Thr Asp Leu Lys Lys Glu Gly Leu Glu Met Lys Ser
1825 1830 1835

<210> 9
<211> 420
<212> DNA
<213> Erwinia amylovora

<400> 9
atgacatcgt cacagcagcg ggttgaaagg tttttacagt atttctccgc cgggtgtaaa 60
acgcccatac atctgaaaga cggggtgtgc gccctgtata acgaacaaga tgaggaggcg 120
gcggtgctgg aagtaccgca acacagcgac agcctgttac tacactgccg aatcattgag 180
gctgaccac aaacttcaat aaccctgtat tcgatgctat tacagctgaa ttttgaaatg 240
gcggccatgc gcggctgttg gctggcgctg gatgaactgc acaacgtgcg tttatgtttt 300
cagcagtcgc tggagcatct ggatgaagca agtttttagcg atatcgttag cggcttcac 360
gaacatgcgg cagaagtgcg tgagtatata gcgcaattag acgagagtag cgcggcataa 420

<210> 10
<211> 139
<212> PRT
<213> Erwinia amylovora

<400> 10
Met Thr Ser Ser Gln Gln Arg Val Glu Arg Phe Leu Gln Tyr Phe Ser
1 5 10 15

Ala Gly Cys Lys Thr Pro Ile His Leu Lys Asp Gly Val Cys Ala Leu
20 25 30

Tyr Asn Glu Gln Asp Glu Glu Ala Ala Val Leu Glu Val Pro Gln His
35 40 45

Ser Asp Ser Leu Leu Leu His Cys Arg Ile Ile Glu Ala Asp Pro Gln
50 55 60

Thr Ser Ile Thr Leu Tyr Ser Met Leu Leu Gln Leu Asn Phe Glu Met
65 70 75 80

Ala Ala Met Arg Gly Cys Trp Leu Ala Leu Asp Glu Leu His Asn Val
85 90 95

Arg Leu Cys Phe Gln Gln Ser Leu Glu His Leu Asp Glu Ala Ser Phe
100 105 110

Ser Asp Ile Val Ser Gly Phe Ile Glu His Ala Ala Glu Val Arg Glu
115 120 125

Tyr Ile Ala Gln Leu Asp Glu Ser Ser Ala Ala
130 135

<210> 11

<211> 341

<212> PRT

<213> Pseudomonas syringae

<400> 11

Met Gln Ser Leu Ser Leu Asn Ser Ser Ser Leu Gln Thr Pro Ala Met
1 5 10 15

Ala Leu Val Leu Val Arg Pro Glu Ala Glu Thr Thr Gly Ser Thr Ser
20 25 30

Ser Lys Ala Leu Gln Glu Val Val Val Lys Leu Ala Glu Glu Leu Met
35 40 45

Arg Asn Gly Gln Leu Asp Asp Ser Ser Pro Leu Gly Lys Leu Leu Ala
50 55 60

Lys Ser Met Ala Ala Asp Gly Lys Ala Gly Gly Gly Ile Glu Asp Val
65 70 75 80

Ile Ala Ala Leu Asp Lys Leu Ile His Glu Lys Leu Gly Asp Asn Phe
85 90 95

Gly Ala Ser Ala Asp Ser Ala Ser Gly Thr Gly Gln Gln Asp Leu Met
100 105 110

Thr Gln Val Leu Asn Gly Leu Ala Lys Ser Met Leu Asp Asp Leu Leu
115 120 125

Thr Lys Gln Asp Gly Gly Thr Ser Phe Ser Glu Asp Asp Met Pro Met
130 135 140

Leu Asn Lys Ile Ala Gln Phe Met Asp Asp Asn Pro Ala Gln Phe Pro
145 150 155 160

Lys Pro Asp Ser Gly Ser Trp Val Asn Glu Leu Lys Glu Asp Asn Phe

	165		170		175
Leu Asp Gly Asp Glu Thr Ala Ala Phe Arg Ser Ala Leu Asp Ile Ile					
	180		185		190
Gly Gln Gln Leu Gly Asn Gln Gln Ser Asp Ala Gly Ser Leu Ala Gly					
	195		200		205
Thr Gly Gly Gly Leu Gly Thr Pro Ser Ser Phe Ser Asn Asn Ser Ser					
	210		215		220
Val Met Gly Asp Pro Leu Ile Asp Ala Asn Thr Gly Pro Gly Asp Ser					
	225		230		235
Gly Asn Thr Arg Gly Glu Ala Gly Gln Leu Ile Gly Glu Leu Ile Asp					
	245		250		255
Arg Gly Leu Gln Ser Val Leu Ala Gly Gly Gly Leu Gly Thr Pro Val					
	260		265		270
Asn Thr Pro Gln Thr Gly Thr Ser Ala Asn Gly Gly Gln Ser Ala Gln					
	275		280		285
Asp Leu Asp Gln Leu Leu Gly Gly Leu Leu Leu Lys Gly Leu Glu Ala					
	290		295		300
Thr Leu Lys Asp Ala Gly Gln Thr Gly Thr Asp Val Gln Ser Ser Ala					
	305		310		315
Ala Gln Ile Ala Thr Leu Leu Val Ser Thr Leu Leu Gln Gly Thr Arg					
	325		330		335
Asn Gln Ala Ala Ala					
	340				

<210> 12
 <211> 1026
 <212> DNA
 <213> Pseudomonas syringae

<400> 12
 atgcagagtc tcagtcttaa cagcagctcg ctgcaaacc cggcaatggc ccttgctctg 60
 gtacgtcctg aagccgagac gactggcagt acgtcgagca aggcgcttca ggaagttgtc 120
 gtgaagctgg ccgaggaact gatgcgcaat ggtcaactcg acgacagctc gccattggga 180
 aaactgttgg ccaagtcgat ggccgcagat ggcaaggcgg gcggcggtat tgaggatgtc 240
 atcgctgcgc tggacaagct gatccatgaa aagctcggtg acaacttcgg cgcgtctgcg 300
 gacagcgcct cgggtaccgg acagcaggac ctgatgactc aggtgctcaa tggcctggcc 360

aagtcgatgc tcgatgatct tctgaccaag caggatggcg ggacaagctt ctccgaagac 420
gatatgccga tgctgaacaa gatcgcgag ttcattgatg acaatcccgc acagtttccc 480
aagccggact cgggtccctg ggtgaacgaa ctcaaggaag acaacttcct tgatggcgac 540
gaaacggctg cgttccgttc ggcaactcgac atcattggcc agcaactggg taatcagcag 600
agtgcgctg gcagtctggc agggacgggt ggaggtctgg gcactccgag cagtttttcc 660
aacaactcgt ccgtgatggg tgatccgctg atcgacgcca ataccgggtcc cggtgacagc 720
ggcaataccc gtggtgaagc ggggcaactg atcggcgagc ttatcgaccg tggcctgcaa 780
tcggtattgg ccggtggtgg actgggcaca cccgtaaaca ccccgagac cggtagctcg 840
gcgaatggcg gacagtccgc tcaggatctt gatcagttgc tgggcggctt gctgctcaag 900
ggcctggagg caacgctcaa ggatgccggg caaacaggca ccgacgtgca gtcgagcgct 960
gcgcaaactc ccaccttgct ggtcagtagc ctgctgcaag gcacccgcaa tcaggctgca 1020
gcctga 1026

<210> 13

<211> 1729

<212> DNA

<213> *Pseudomonas syringae*

<400> 13

tccacttcgc tgattttgaa attggcagat tcatagaaac gttcaggtgt ggaaatcagg 60
ctgagtgcgc agatttcggt gataaggggtg tggtagtggc cattgttggc cattttcaagg 120
cctctgagtg cgggtgcggag caataccagt cttcctgctg gcgtgtgcac actgagtcgc 180
aggcataggc atttcagttc cttgcgttgg ttgggcataa aaaaaaagga acttttaaaa 240
acagtgcaat gagatgccgg caaaacggga accggtcgct gcgctttgcc actcacttcg 300
agcaagctca accccaaaca tccacatccc tatcgaacgg acagcgatac ggccacttgc 360
tctggtaaac cctggagctg gcgtcgggtcc aattgcccac ttagcgaggc aacgcagcat 420
gagcatcggc atcacacccc ggccgcaaca gaccaccacg ccaactcgatt ttctggcgct 480
aagcggcaag agtccctaac caaacacgtt cggcgagcag aacactcagc aagcgatoga 540
cccagtgca ctgttgcttc gcagcgacac acagaaagac gtcaacttcg gcacgcccga 600
cagcaccgtc cagaatccgc aggacgccag caagcccaac gacagccagt ccaacatcgc 660
taaattgatc agtgcattga tcatgtcggt gctgcagatg ctcaccaact ccaataaaaa 720
gcaggacacc aatcaggaac agcctgatag ccaggctcct ttccagaaca acggcgggct 780
cggtagaccg tcggccgata gcggggcgcg cggtagaccg gatgcgacag gtggcgggcg 840
cggtagatcg ccaagcgcaa caggcggtgg cggcggtgat actccgaccg caacaggcg 900
tgccggcagc ggtggcgcg gcacacccac tgcaacaggg ggccggcagcg gtggcacacc 960
cactgcaaca ggcggtggcg aggggtggcg aacacggcaa atcactccgc agttggccaa 1020
ccctaaccgt acctcaggtg ctggctcggt gtcggacacc gcaggttcta ccgagcaagc 1080
cggcaagatc aatgtggtga aagacaccat caaggctcggc gctggcgaag tctttgacgg 1140
ccacggcgca accttcactg ccgacaaatc tatgggtaac ggagaccagg gcgaaaatca 1200
gaagcccatg ttcgagctgg ctgaaggcgc tacgttgaag aatgtgaacc tgggtgagaa 1260
cgaggtcgat ggcattccag tgaaagccaa aaacgctcag gaagtcacca ttgacaacgt 1320
gcatgccag aacgtcgggt aagacctgat tacggtcaaa ggcgaggag gcgcagcggt 1380
cactaatctg aacatcaaga acagcagtcg caaagggtgca gacgacaagg ttgtccagct 1440
caacgccaac actcacttga aaatcgacaa cttcaaggcc gacgatttcg gcacgatggc 1500
tcgacccaac ggtggcaagc agttttgatg catgagcatc gagctgaacg gcatcgaagc 1560
taaccacggc aagttcgccc tggtgaaaag cgacagtgac gatctgaagc tggcaacggg 1620
caacatcgcc atgacggagc tcaaacacgc ctacgataaa acccaggcat cgacccaaca 1680

caccgagctt tgaatccaga caagtagctt gaaaaaaggg ggtggactc

1729

<210> 14

<211> 424

<212> PRT

<213> *Pseudomonas syringae*

<400> 14

Met Ser Ile Gly Ile Thr Pro Arg Pro Gln Gln Thr Thr Thr Pro Leu
1 5 10 15

Asp Phe Ser Ala Leu Ser Gly Lys Ser Pro Gln Pro Asn Thr Phe Gly
20 25 30

Glu Gln Asn Thr Gln Gln Ala Ile Asp Pro Ser Ala Leu Leu Phe Gly
35 40 45

Ser Asp Thr Gln Lys Asp Val Asn Phe Gly Thr Pro Asp Ser Thr Val
50 55 60

Gln Asn Pro Gln Asp Ala Ser Lys Pro Asn Asp Ser Gln Ser Asn Ile
65 70 75 80

Ala Lys Leu Ile Ser Ala Leu Ile Met Ser Leu Leu Gln Met Leu Thr
85 90 95

Asn Ser Asn Lys Lys Gln Asp Thr Asn Gln Glu Gln Pro Asp Ser Gln
100 105 110

Ala Pro Phe Gln Asn Asn Gly Gly Leu Gly Thr Pro Ser Ala Asp Ser
115 120 125

Gly Gly Gly Gly Thr Pro Asp Ala Thr Gly Gly Gly Gly Gly Asp Thr
130 135 140

Pro Ser Ala Thr Gly Gly Gly Gly Gly Asp Thr Pro Thr Ala Thr Gly
145 150 155 160

Gly Gly Gly Ser Gly Gly Gly Gly Thr Pro Thr Ala Thr Gly Gly Gly
165 170 175

Ser Gly Gly Thr Pro Thr Ala Thr Gly Gly Gly Glu Gly Gly Val Thr
180 185 190

Pro Gln Ile Thr Pro Gln Leu Ala Asn Pro Asn Arg Thr Ser Gly Thr
195 200 205

0907940-06400

<400> 15

Met Ser Val Gly Asn Ile Gln Ser Pro Ser Asn Leu Pro Gly Leu Gln
1 5 10 15

Asn Leu Asn Leu Asn Thr Asn Thr Asn Ser Gln Gln Ser Gly Gln Ser
20 25 30

Val Gln Asp Leu Ile Lys Gln Val Glu Lys Asp Ile Leu Asn Ile Ile
35 40 45

Ala Ala Leu Val Gln Lys Ala Ala Gln Ser Ala Gly Gly Asn Thr Gly
50 55 60

Asn Thr Gly Asn Ala Pro Ala Lys Asp Gly Asn Ala Asn Ala Gly Ala
65 70 75 80

Asn Asp Pro Ser Lys Asn Asp Pro Ser Lys Ser Gln Ala Pro Gln Ser
85 90 95

Ala Asn Lys Thr Gly Asn Val Asp Asp Ala Asn Asn Gln Asp Pro Met
100 105 110

Gln Ala Leu Met Gln Leu Leu Glu Asp Leu Val Lys Leu Leu Lys Ala
115 120 125

Ala Leu His Met Gln Gln Pro Gly Gly Asn Asp Lys Gly Asn Gly Val
130 135 140

Gly Gly Ala Asn Gly Ala Lys Gly Ala Gly Gly Gln Gly Gly Leu Ala
145 150 155 160

Glu Ala Leu Gln Glu Ile Glu Gln Ile Leu Ala Gln Leu Gly Gly Gly
165 170 175

Gly Ala Gly Ala Gly Gly Ala Gly Gly Gly Val Gly Gly Ala Gly Gly
180 185 190

Ala Asp Gly Gly Ser Gly Ala Gly Gly Ala Gly Gly Ala Asn Gly Ala
195 200 205

Asp Gly Gly Asn Gly Val Asn Gly Asn Gln Ala Asn Gly Pro Gln Asn
210 215 220

Ala Gly Asp Val Asn Gly Ala Asn Gly Ala Asp Asp Gly Ser Glu Asp
225 230 235 240

Gln Gly Gly Leu Thr Gly Val Leu Gln Lys Leu Met Lys Ile Leu Asn
245 250 255

Ala Leu Val Gln Met Met Gln Gln Gly Gly Leu Gly Gly Gly Asn Gln
 260 265 270

Ala Gln Gly Gly Ser Lys Gly Ala Gly Asn Ala Ser Pro Ala Ser Gly
 275 280 285

Ala Asn Pro Gly Ala Asn Gln Pro Gly Ser Ala Asp Asp Gln Ser Ser
 290 295 300

Gly Gln Asn Asn Leu Gln Ser Gln Ile Met Asp Val Val Lys Glu Val
 305 310 315 320

Val Gln Ile Leu Gln Gln Met Leu Ala Ala Gln Asn Gly Gly Ser Gln
 325 330 335

Gln Ser Thr Ser Thr Gln Pro Met
 340

<210> 16

<211> 1035

<212> DNA

<213> Pseudomonas solanacearum

<400> 16

atgtcagtcg gaaacatcca gagcccgtcg aacctcccgg gtctgcagaa cctgaacctc 60
 aacaccaaca ccaacagcca gcaatcgggc cagtcogtgc aagacctgat caagcaggtc 120
 gagaaggaca tcctcaacat catcgcagcc ctcgtgcaga aggccgcaca gtcggcgggc 180
 ggcaacaccg gtaacaccgg caacgcgccg gcgaaggacg gcaatgccaa cgcggggcgcc 240
 aacgacccga gcaagaacga cccgagcaag agccaggctc cgcagtcggc caacaagacc 300
 ggcaacgtcg acgacgcaa caaccaggat ccgatgcaag cgctgatgca gctgctggaa 360
 gacctggtga agctgctgaa ggcgggccctg cacatgcagc agcccggcgg caatgacaag 420
 ggcaacggcg tggcggtgc caacggcgcc aagggtgccg gcggccaggg cggcctggcc 480
 gaagcgctgc aggagatcga gcagatcctc gccagctcg gcggcgccgg tgcctggcgcc 540
 ggcgggcgcg gtggcggtgt cggcggtgct ggtggcgcg atggcggtc cggcgcggt 600
 ggcgaggcg gtgcgaacgg cgccgacggc ggcaatggcg tgaacggcaa ccaggcgaac 660
 ggcccgcaga acgcaggcga tgtcaacggt gccaacggcg cggatgacgg cagcgaagac 720
 caggcgcgcc tcaccggcgt gctgcaaaag ctgatgaaga tcctgaacgc gctggtgcag 780
 atgatgcagc aaggcggcct cggcgggcgc aaccaggcgc agggcggtc gaagggtgcc 840
 ggcaacgcct cgccggcttc cggcggaac cggggcgga accagcccg ttcggcggat 900
 gatcaatcgt ccggccagaa caatctgcaa tcccagatca tggatgtggt gaaggaggtc 960
 gtccagatcc tgcagcagat gctggcgggc cagaacggcg gcagccagca gtccacctcg 1020
 acgcagccga tgtaa 1035

<210> 17

<211> 10

